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Structural Constraints on Protein Autoprocessings through an N-O or N-S Acyl Shift. Y. Sun, Y. Wang, H.-C. Guo, Dept. of Physiology and Biophysics, Boston Univ. School of Medicine, Boston, MA 02118 USA.

Proteolysis is involved in activating many biological functions. A unique type of proteolysis, protein autoprocessing, has emerged as novel mechanism of posttranslational modification. It is initiated by a nucleophilic attack of a threonine, serine, or cysteine residue at the scissile peptide bond, leading to an N-O or N-S acyl shift. From that intermediate, a diverse group of proteins undergo various types of peptide-bond rearrangements. Intramolecular autoproteolysis is one such novel mechanism found to activate human nucleoporin hNup98 and glycosylasparaginase (GA). We have determined precursor structures of the *Flavobacterium* GA and hNup98 autoproteolytic domain, both at 1.9 Å resolution. Interestingly, structural constraints are found near the scissile peptide bonds of both precursors. Structural comparisons of these two precursor structures are underway to study mechanistic similarities and differences between them.